



GZ 2094.00 Sequence Listing
SEQUENCE LISTING

<110> Nicolette, Charles

<120> THERAPEUTIC ANTI-MELANOMA COMPOUNDS

<130> GZ 2094.00

<140> 09/812,238

<141> 2001-03-19

<160> 19

<170> FastSEQ for windows Version 3.0

<210> 1

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)...(2004)

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Met Asp Leu Val Leu Lys Arg Cys Leu Leu	
1 5 10	
cat ttg gct gtg ata ggt gct ttg ctg gct gtg ggg gct aca aaa gta	99
His Leu Ala Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr Lys Val	
15 20 25	
ccc aga aac cag gac tgg ctt ggt gtc tca agg caa ctc aga acc aaa	147
Pro Arg Asn Gln Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Thr Lys	
30 35 40	
gcc tgg aac agg cag ctg tat cca gag tgg aca gaa gcc cag aga ctt	195
Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu	
45 50 55	
gac tgc tgg aga ggt ggt caa gtg tcc ctc aag gtc agt aat gat ggg	243
Asp Cys Trp Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn Asp Gly	
60 65 70	
cct aca ctg att ggt gca aat gcc tcc ttc tct att gcc ttg aac ttc	291
Pro Thr Leu Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe	
75 80 85 90	
cct gga agc caa aag gta ttg cca gat ggg cag gtt atc tgg gtc aac	339
Pro Gly Ser Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Val Asn	
95 100 105	
aat acc atc atc aat ggg agc cag gtg tgg gga gga cag cca gtg tat	387
Asn Thr Ile Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro Val Tyr	
110 115 120	
ccc cag gaa act gac gat gcc tgc atc ttc cct gat ggt gga cct tgc	435
Pro Gln Glu Thr Asp Asp Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys	
125 130 135	
cca tct ggc tct tgg tct cag aag aga agc ttt gtt tat gtc tgg aag	483

GZ 2094.00 Sequence Listing

Pro	Ser	Gly	Ser	Trp	Ser	Gln	Lys	Arg	Ser	Phe	Val	Tyr	Val	Trp	Lys	
140						145					150					
acc	tgg	ggc	caa	tac	tgg	caa	gtt	cta	ggg	ggc	cca	gtg	tct	ggg	ctg	531
Thr	Trp	Gly	Gln	Tyr	Trp	Gln	Val	Leu	Gly	Gly	Pro	Val	Ser	Gly	Leu	
155					160				165						170	
agc	att	ggg	aca	ggc	agg	gca	atg	ctg	ggc	aca	cac	acc	atg	gaa	gtg	579
Ser	Ile	Gly	Thr	Gly	Arg	Ala	Met	Leu	Gly	Thr	His	Thr	Met	Glu	Val	
				175					180					185		
act	gtc	tac	cat	cgc	cgg	gga	tcc	cgg	agc	tat	gtg	cct	ctt	gct	cat	627
Thr	Val	Tyr	His	Arg	Arg	Gly	Ser	Arg	Ser	Tyr	Val	Pro	Leu	Ala	His	
			190					195					200			
tcc	agc	tca	gcc	ttc	acc	att	act	gac	cag	gtg	cct	ttc	tcc	gtg	agc	675
Ser	Ser	Ser	Ala	Phe	Thr	Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser	Val	Ser	
			205				210					215				
gtg	tcc	cag	ttg	cgg	gcc	ttg	gat	gga	ggg	aac	aag	cac	ttc	ctg	aga	723
Val	Ser	Gln	Leu	Arg	Ala	Leu	Asp	Gly	Gly	Asn	Lys	His	Phe	Leu	Arg	
	220					225					230					
aat	cag	cct	ctg	acc	ttt	gcc	ctc	cag	ctc	cat	gac	ccc	agt	ggc	tat	771
Asn	Gln	Pro	Leu	Thr	Phe	Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	
235					240					245					250	
ctg	gct	gaa	gct	gac	ctc	tcc	tac	acc	tgg	gac	ttt	gga	gac	agt	agt	819
Leu	Ala	Glu	Ala	Asp	Leu	Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp	Ser	Ser	
				255					260					265		
gga	acc	ctg	atc	tct	cgg	gca	ctt	gtg	gtc	act	cat	act	tac	ctg	gag	867
Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Val	Val	Thr	His	Thr	Tyr	Leu	Glu	
			270					275					280			
cct	ggc	cca	gtc	act	gcc	cag	gtg	gtc	ctg	cag	gct	gcc	att	cct	ctc	915
Pro	Gly	Pro	Val	Thr	Ala	Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	
			285				290					295				
acc	tcc	tgt	ggc	tcc	tcc	cca	gtt	cca	ggc	acc	aca	gat	ggg	cac	agg	963
Thr	Ser	Cys	Gly	Ser	Ser	Pro	Val	Pro	Gly	Thr	Thr	Asp	Gly	His	Arg	
	300					305					310					
cca	act	gca	gag	gcc	cct	aac	acc	aca	gct	ggc	caa	gtg	cct	act	aca	1011
Pro	Thr	Ala	Glu	Ala	Pro	Asn	Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	
315					320					325					330	
gaa	gtt	gtg	ggt	act	aca	cct	ggt	cag	gcg	cca	act	gca	gag	ccc	tct	1059
Glu	Val	Val	Gly	Thr	Thr	Pro	Gly	Gln	Ala	Pro	Thr	Ala	Glu	Pro	Ser	
				335					340					345		
gga	acc	aca	tct	gtg	cag	gtg	cca	acc	act	gaa	gtc	ata	agc	act	gca	1107
Gly	Thr	Thr	Ser	Val	Gln	Val	Pro	Thr	Thr	Glu	Val	Ile	Ser	Thr	Ala	
			350					355					360			
cct	gtg	cag	atg	cca	act	gca	gag	agc	aca	ggt	atg	aca	cct	gag	aag	1155
Pro	Val	Gln	Met	Pro	Thr	Ala	Glu	Ser	Thr	Gly	Met	Thr	Pro	Glu	Lys	
			365				370					375				
gtg	cca	gtt	tca	gag	gtc	atg	ggt	acc	aca	ctg	gca	gag	atg	tca	act	1203
Val	Pro	Val	Ser	Glu	Val	Met	Gly	Thr	Thr	Leu	Ala	Glu	Met	Ser	Thr	
	380					385						390				

GZ 2094.00 Sequence Listing

cca gag gct aca ggt atg aca cct gca gag gta tca att gtg gtg ctt	1251
Pro Glu Ala Thr Gly Met Thr Pro Ala Glu Val Ser Ile Val Val Leu	
395 400 405 410	
tct gga acc aca gct gca cag gta aca act aca gag tgg gtg gag acc	1299
Ser Gly Thr Thr Ala Ala Gln Val Thr Thr Thr Glu Trp Val Glu Thr	
415 420 425	
aca gct aga gag cta cct atc cct gag cct gaa ggt cca gat gcc agc	1347
Thr Ala Arg Glu Leu Pro Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser	
430 435 440	
tca atc atg tct acg gaa agt att aca ggt tcc ctg ggc ccc ctg ctg	1395
Ser Ile Met Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu	
445 450 455	
gat ggt aca gcc acc tta agg ctg gtg aag aga caa gtc ccc ctg gat	1443
Asp Gly Thr Ala Thr Leu Arg Leu Val Lys Arg Gln Val Pro Leu Asp	
460 465 470	
tgt gtt ctg tat cga tat ggt tcc ttt tcc gtc acc ctg gac att gtc	1491
Cys Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val Thr Leu Asp Ile Val	
475 480 485 490	
cag ggt att gaa agt gcc gag atc ctg cag gct gtg ccg tcc ggt gag	1539
Gln Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser Gly Glu	
495 500 505	
ggg gat gca ttt gag ctg act gtg tcc tgc caa ggc ggg ctg ccc aag	1587
Gly Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys	
510 515 520	
gaa gcc tgc atg gag atc tca tcg cca ggg tgc cag ccc cct gcc cag	1635
Glu Ala Cys Met Glu Ile Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln	
525 530 535	
cgg ctg tgc cag cct gtg cta ccc agc cca gcc tgc cag ctg gtt ctg	1683
Arg Leu Cys Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu Val Leu	
540 545 550	
cac cag ata ctg aag ggt ggc tcg ggg aca tac tgc ctc aat gtg tct	1731
His Gln Ile Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser	
555 560 565 570	
ctg gct gat acc aac agc ctg gca gtg gtc agc acc cag ctt atc atg	1779
Leu Ala Asp Thr Asn Ser Leu Ala Val Val Ser Thr Gln Leu Ile Met	
575 580 585	
cct ggt caa gaa gca ggc ctt ggg cag gtt ccg ctg atc gtg ggc atc	1827
Pro Gly Gln Glu Ala Gly Leu Gly Gln Val Pro Leu Ile Val Gly Ile	
590 595 600	
ttg ctg gtg ttg atg gct gtg gtc ctt gca tct ctg ata tat agg cgc	1875
Leu Leu Val Leu Met Ala Val Val Leu Ala Ser Leu Ile Tyr Arg Arg	
605 610 615	
aga ctt atg aag caa gac ttc tcc gta ccc cag ttg cca cat agc agc	1923
Arg Leu Met Lys Gln Asp Phe Ser Val Pro Gln Leu Pro His Ser Ser	
620 625 630	
agt cac tgg ctg cgt cta ccc cgc atc ttc tgc tct tgt ccc att ggt	1971
Ser His Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly	
635 640 645 650	

GZ 2094.00 Sequence Listing

gag aat agc ccc ctc ctc agt ggg cag gtc tgagtactct catatgatgc 2024
 Glu Asn Ser Pro Leu Leu Ser Gly Gln Val
 655 660

tgtgattttc ctggagttga cagaaacacc tatattttccc ccagtctttcc ctgggagact 2084
 actattaact gaaataaata ctcagagcct gaaaaaaaaa aaaaaa 2130

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 35 40 45
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
 50 55 60
 Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
 65 70 75 80
 Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
 100 105 110
 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
 115 120 125
 Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
 130 135 140
 Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
 145 150 155 160
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
 165 170 175
 Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
 180 185 190
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
 195 200 205
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
 210 215 220
 Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
 225 230 235 240
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
 245 250 255
 Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
 260 265 270
 Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
 275 280 285
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
 290 295 300
 Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
 305 310 315 320
 Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
 325 330 335
 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
 340 345 350
 Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
 355 360 365
 Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
 370 375 380
 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met

GZ 2094.00 Sequence Listing

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385      390      395      400
Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
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Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
420      425      430
Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
435      440      445
Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
450      455      460
Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
465      470      475      480
Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
485      490      495
Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
500      505      510
Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
515      520      525
Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
530      535      540
Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
545      550      555      560
Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
565      570      575
Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly
580      585      590
Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala
595      600      605
Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp
610      615      620
Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu
625      630      635      640
Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu
645      650      655
Ser Gly Gln Gln Val
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<210> 3
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<210> 4
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 <223> n= A, T, C or G

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GZ 2094.00 Sequence Listing

<400> 5
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GZ 2094.00 Sequence Listing

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GZ 2094.00 Sequence Listing

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<210> 18
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<210> 19
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 <212> PRT
 <213> Homo sapiens

<400> 19
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 1 5